

**AMENDMENTS TO THE CLAIMS**

**This listing of claims will replace all prior versions and listings of claims in the application:**

**LISTING OF CLAIMS:**

1-17. (canceled).

18. (previously presented): A method of obtaining isolated selected mRNA species or isolated selected cDNA species useful for diagnosing or identifying breast cancer in a human comprising the steps of:

- (a) isolating mRNA from cells from blood of more than one human who are known to have very early stage breast cancer (breast cancer sample), wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA;
- (b) isolating mRNA from corresponding cells from blood of more than one normal human (normal sample), wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA;
- (c) separating mRNA species or cDNA species present within each of the resulting isolated mRNA or isolated cDNA of step (a) and step (b), wherein the resulting separated mRNA species are optionally subject to reverse transcription to obtain separated cDNA species;
- (d) selecting 10 or more mRNA species or 10 or more cDNA species from the resulting separated mRNA species or resulting separated cDNA species obtained in step (c), respectively, which are present at a different level in the normal sample than in the breast cancer sample by identifying a signal corresponding to each mRNA species or cDNA species, wherein the resulting selected 10 or more mRNA species are optionally subjected to reverse transcription to obtain 10 or more selected cDNA species; and
- (e) isolating the resulting 10 or more selected mRNA species or resulting 10 or more selected cDNA species obtained in step (d) to obtain isolated

selected mRNA species or isolated selected cDNA species, wherein the resulting isolated selected mRNA species are optionally subjected to reverse transcription to obtain isolated selected cDNA species.

19. (previously presented): A method of preparing a gene transcript pattern probe kit comprising the steps of:

- (a) isolating mRNA from cells from blood of more than one human who are known to have very early stage breast cancer (breast cancer sample), wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA;
- (b) isolating mRNA from corresponding cells from blood of more than one normal human (normal sample), wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA;
- (c) separating mRNA species or cDNA species present within each of the resulting isolated mRNA or isolated cDNA of step (a) and step (b), wherein the resulting separated mRNA species are optionally subject to reverse transcription to obtain separated cDNA species;
- (d) selecting 10 or more mRNA species or 10 or more cDNA species from the resulting separated mRNA species or resulting separated cDNA species obtained in step (c) respectively, which are present at a different level in the normal sample than in the breast cancer sample by identifying a signal corresponding to each mRNA species or cDNA species, wherein the resulting selected 10 or more mRNA species are optionally subjected to reverse transcription to obtain 10 or more selected cDNA species;
- (e) isolating the resulting 10 or more selected mRNA species or resulting 10 or more selected cDNA species obtained in step (d) to obtain isolated selected mRNA species or isolated selected cDNA species, wherein the resulting isolated selected mRNA species are optionally subjected to reverse transcription to obtain isolated selected cDNA species; and

- (f) preparing at least one solid support carrying the resulting isolated selected mRNA species or isolated selected cDNA species of step (e) so as to form a gene transcript pattern probe kit.

20. (previously presented): The method as claimed in claim 18 or 19, wherein said separation in step (c) is performed by a non-sequence based separation technique.

21. (previously presented): The method as claimed in claim 18 or 19, wherein in steps (a) and (b), the resulting isolated mRNA is subjected to reverse transcription to obtain isolated cDNA.

22. (previously presented): The method as claimed in claim 21, wherein said isolated cDNA is amplified.

23. (previously presented): The method as claimed in claim 18 or 19, wherein in step (e), between 50 and 100 mRNA species or cDNA species are isolated and selected.

24. (previously presented): The method as claimed in claim 18 or 19, wherein, in step (e) between 10 and 500 mRNA species or cDNA species are isolated and selected.

25. (previously presented): The method as claimed in claim 18 or 19, wherein, in step (c), said separation technique is gel electrophoresis.

26. (previously presented): The method as claimed in claim 19, wherein, prior to immobilizing in step (f), the resulting isolated selected mRNA species or isolated selected cDNA species of step (e) are amplified.

27. (currently amended): A method of preparing a standard gene transcript pattern characteristic of breast cancer of a human comprising the steps of:

- (a) isolating mRNA from cells from blood of more than one human who are known to have said breast cancer (breast cancer sample), wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA;
- (b) isolating 10 or more mRNA or cDNA species which are specific for said breast cancer and are present at a different level in cells in a blood sample from more than one normal human than in corresponding cells in a blood sample from more than one human who are known to have very early stage breast cancer according to the method of claim 18;
- ~~(b)~~ hybridizing the resulting isolated mRNA or isolated cDNA of step (a) to said 10 or more mRNA or cDNA species of step (b)~~which are present at a different level in cells in a blood sample from more than one normal human than in corresponding cells in a blood sample from more than one human who are known to have very early stage breast cancer, or to 10 or more cDNA species transcribed from said mRNA species, wherein the 10 or more mRNA species or cDNA species are specific for said breast cancer, wherein said mRNA or cDNA species of step (b) are carried on a solid support; and~~
- ~~(e)~~ assessing the amount of hybridization so as to obtain said standard gene transcript pattern.

28. (currently amended): A method of preparing a test gene transcript pattern for breast cancer in a human comprising the steps of:

- (a) isolating mRNA from cells from blood of a test human suspected to have breast cancer, wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA;
- (b) isolating 10 or more mRNA or cDNA species which are specific for said breast cancer and are present at a different level in cells in a blood sample from more than one normal human than in corresponding cells in a blood sample from more than one human who are known to have very early stage breast cancer according to the method of claim 18;

- (~~b~~c) hybridizing the resulting isolated mRNA or isolated cDNA of step (a) to said 10 or more mRNA or cDNA species of step (b)~~which are present at a different level in cells in a blood sample from more than one normal human than in corresponding cells in a blood sample from more than one human who are known to have very early stage breast cancer, or to 10 or more cDNA species transcribed from said mRNA species, wherein the 10 or more mRNA species or cDNA species are specific for said breast cancer, wherein said mRNA or cDNA species of step (b) are carried on a solid support; and~~
- (~~e~~d) assessing the amount of hybridization so as to obtain said test gene transcript pattern.

29. (currently amended): A method of diagnosing or identifying breast cancer in a test human comprising the steps of:

- (a) isolating mRNA from cells from blood of a test human, wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA;
- (~~b~~) isolating 10 or more mRNA or cDNA species which are specific for said breast cancer according to the method of claim 18;
- (~~b~~c) hybridizing the resulting isolated mRNA or isolated cDNA of step (a) to 10 or more mRNA or cDNA species of step (b)~~which are present at a different level in cells in a blood sample from more than one normal human than in corresponding cells in a blood sample from more than one human who are known to have very early stage breast cancer, or to 10 or more cDNA species transcribed from said mRNA species, wherein the 10 or more mRNA species or cDNA species are specific for said breast cancer, wherein said mRNA or cDNA species of step (b) are carried on a solid support;~~
- (~~d~~) hybridizing isolated mRNA or isolated cDNA prepared from corresponding cells from blood of more than one human who are known to have said breast cancer to the 10 or more mRNA or cDNA species of step

(b) wherein said mRNA species or cDNA species of step (b) are carried on a solid support;

- (ee) assessing the amount of hybridization in steps (c) and (d) so as to obtain a test and standard hybridization pattern; and
- (df) ~~comparing the resulting hybridization patterns obtained in step (ee) with a hybridization pattern obtained by hybridizing isolated mRNA or isolated cDNA prepared from corresponding cells from blood of more than one human who are known to have said breast cancer to the 10 or more mRNA species or 10 or more cDNA species transcribed from said mRNA species, wherein said mRNA species or cDNA species are carried on a solid support,~~ so as to determine the degree of correlation indicative of the presence of said breast cancer, and so as to diagnose or identify said breast cancer in said test human

wherein the mRNA or cDNA species identified in step (b) are present at a different level in cells in a blood sample from more than one normal human than in corresponding cells in a blood sample from more than one human who are known to have very early stage breast cancer.

30. (previously presented): The method as claimed in claim 27, 28 or 29, wherein in step (a), the resulting isolated mRNA is subjected to reverse transcription to obtain isolated cDNA.

31. (previously presented): The method as claimed in claim 30, wherein said isolated cDNA is amplified.

32. (currently amended): The method as claimed in claim 18, 19, 27, 28 or 29, wherein when isolated cDNA is obtained, any of said isolated cDNA is labeled.

33. (currently amended): The method as claimed in claim 27, 28 or 29, wherein, in step (bc), between 50 and 100 mRNA species or cDNA species are used.

34. (currently amended): The method as claimed in claim 27, 28 or 29, wherein, in step (b~~c~~), between 10 and 500 mRNA species or cDNA species are used.

35. (previously presented): The method as claimed in claim 19, 27, 28 or 29, wherein said solid support is a filter.

36-38. (canceled).